

5' TGG CCC CTG GAC ACC TCT GTC ACC ATG TGG TTC CTG GTT CTG TGC CTC GCC CTG
M W F L V L C L A L

TCC CTG GGG GGG ACT GGT GCT GCG CCC CCG ATT CAG TCC CGG ATT GTG GGA GGC
S L G G T G A A P P I Q S R I V G G

TGG GAG TGT GAG CAG CAT TCC CAG CCC TGG CAG GCG GCT CTG TAC CAG AAG ACG
W E C E Q H S Q P W Q A A L Y Q K T

CGG CTA CTC TGT GGG GCG ACG NTC ATN GCC CCC AGA TGG TTC CTG ACA GCA GCC
R L L C G A T X X A P R W F L T A A

CAC TGC CTN AAG CCC CGC TAC ATA GTT CAC CTG GGG CAG CAC AAC CTC CAG AAG
H C L K P R Y I V H L G Q H N L Q K

GAG GAG GGC TGT GAG CAG ACC CGG ACA GCC ACT GAG TCC TTC CCC CAC CCC GGC
E E G C E Q T R T A T E S F P H P G

TTC AAC AAC AGC CTC CCC AAC AAA GAC CAC CGC AAT GAC ATC ATG CTG GTG AAG
F N N S L P N K D H R N D I M L V K

ATG GCA TCG CCA GTC TCC ATC ACC TGG GCT GTG CGA CCC CTC ACC CTC TCC TCA
M A S P V S I T W A V R P L T L S S

CGC TGT GTC ACT GCT GGC ACC AGC TGC CTC ATT TCC GGC TGG GGC AGC ACG TCC
R C V T A G T S C L I S G W G S T S

AGC CCC CAG TTA CGC CTG CCT CAC ACC TTG CGA TGC GCC AAC ATC ACC ATC ATT
S P Q L R L P H T L R C A N I T I I

GAG CAC CAG AAG TGT GAG AAC GCC TAC CCC GGC AAC ATC ACA GAC ACC ATG GTG
E H Q K C E N A Y P G N I T D T M V

TGT GCC AGC GTG CAG GAA GGG GGC AAG GAC TCC TGC CAG GGT GAC TCC GGG GGC
C A S V Q E G G K D S C Q G D S G G

CCT CTG GTC TGT AAC CAG TCT CTT CAA GGC ATT ATC TCC TGG GGC CAG GAT CCG
P L V C N Q S L Q G I I S W G Q D P

FIGURE 1A

		713			722			731			740			749			758
TGT	GCG	ATC	ACC	CGA	AAG	CCT	GGT	GTC	TAC	ACG	AAA	GTC	TGC	AAA	TAT	GTG	GAC
C	A	I	T	R	K	P	G	V	Y	T	K	V	C	K	Y	V	D
		767			776			785			794			803			812
TGG	ATC	CAG	GAG	ACG	ATG	AAG	AAC	AAT	TAG	ACT	GGA	CNT	CAC	CTC	CGA	ANC	CCC
W	I	Q	E	T	M	K	N	N									
		821			830												
CAC	AGC	CCA	TCA	CCC	TCC	ATT	3'										

FIGURE 1B

0860260

1	MWFLVLCLALSLGGTGAAPPPIQSRIVGGWE	SEQ ID NO-1
1	MWFLVLCLALSLGGTGAAPPPIQSRIVGGWE	GI 186653
1	MWFLILFLALFLGGIDAAPPVQSRILIGGFN	GI 55527
31	CEQHSQPWQAALYQKTRL LCGATXXAPRW F	SEQ ID NO-1
31	CEQHSQPWQAALYH FSTFQCGGI L VHRQWV	GI 186653
31	CEKNSQPWHVA VYRFAR YQCGGV LLDANWV	GI 55527
61	LTAAHCL KPRYIVHLGQHNLQKEE GCEQ TR	SEQ ID NO-1
61	LTAAHCL ISDNYQLWLGRHNLFD DENTAQFV	GI 186653
61	LTAAHCL YNDKYQVWL GKNNRFEDEPSAQHQ	GI 55527
91	TAT ESFPHPGFNNSLP N KDH - - - - - R N	SEQ ID NO-1
91	HV S ESFPHPGFNMSLL E - N H T R Q A D E D Y S H	GI 186653
91	LI S K A I P H P G F N M S L L N K D H T P H P E D D Y S N	GI 55527
113	DIMLVKMA SPV - SITWAVRPL T LSSRCVTA	SEQ ID NO-1
120	DLMLLRLTEPADTITDAVKVVELPTQEPEV	GI 186653
121	DLMLVRLKKPAE - ITDVVKPIDLPTEEPTV	GI 55527
142	GTSCLISGWGSTSSPO - LRLPH T L R C A N I T	SEQ ID NO-1
150	GSTCLASGWGSTIEP - ENF S F P D D L Q C V D L K	GI 186653
150	GSRCCLASGWGSTTPTTEEF E Y S H D L O C V Y L E	GI 55527
171	IIEHQK CENAYPGNITDTMVCA SVQEGGKD	SEQ ID NO-1
179	ILPNDECEKAHVQKVTD F M L C V G H L E G G K D	GI 186653
180	LLSNEVC AKAHTEKVTDTMLCAGEMDGGKD	GI 55527
201	SCQGDSSGGPLV C N Q S L Q G I I S W G Q D P C A I T	SEQ ID NO-1
209	TCVGDSSGGPLM C D G V L Q G V T S W G Y V P C G T P	GI 186653
210	TCVGDSSGGPLI C D G V L O G I T S W G P T P C A L P	GI 55527
231	RKPGVYTKV C K Y V D W I Q E T M K N N	SEQ ID NO-1
239	NKPSVAVRV L S Y V K W I E D T I A E N S	GI 186653
240	NVPGIYTKL I E Y R S W I K D V M A N N P	GI 55527

FIGURE 2

061017 0850Z FEB 60

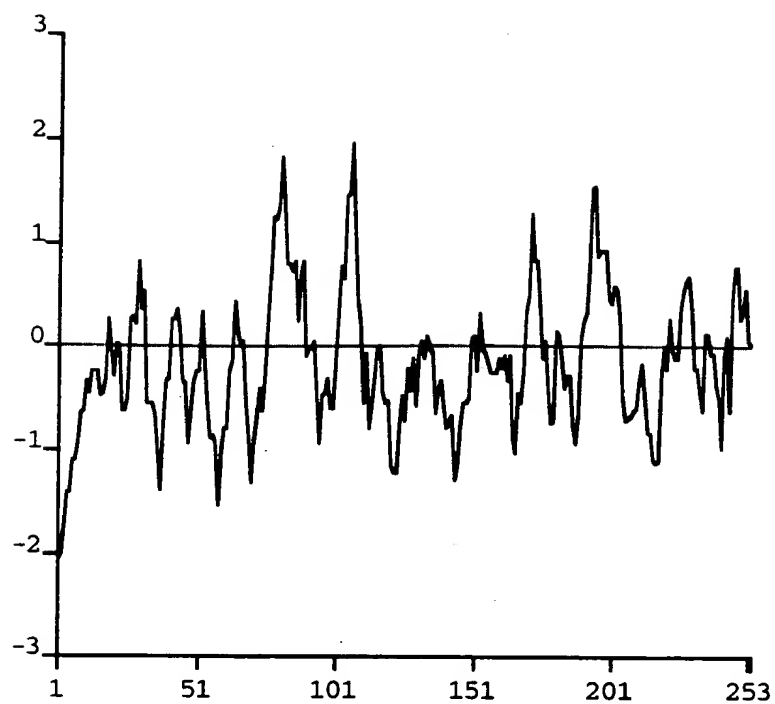


FIGURE 3

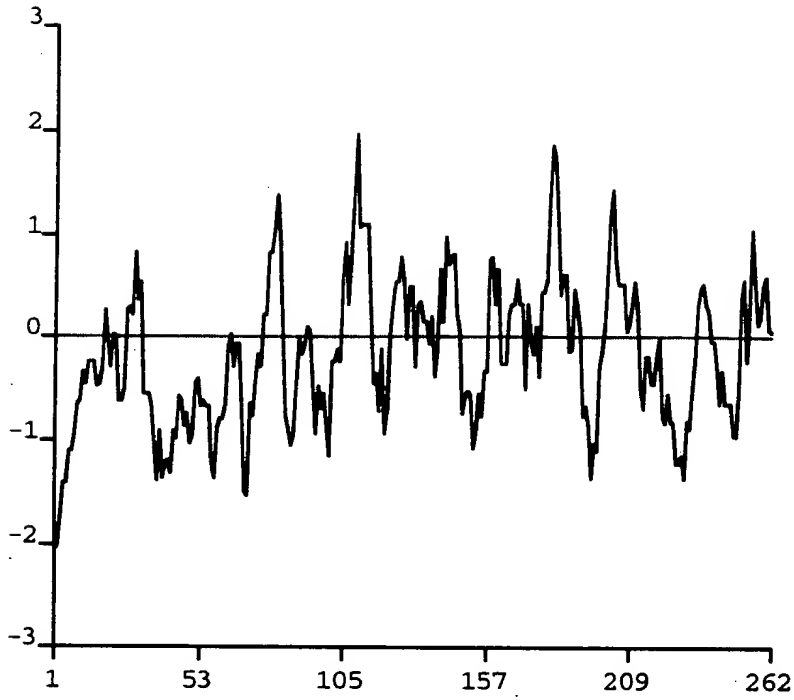


FIGURE 4

Library	Lib Description	Abun	Pct	Abun
PROSNOT19	prostate, 59 M	3	0.0815	
PANCN0T04	pancreas, 5 M	4	0.0675	
LPARN0T02	parotid gland, 70 M	2	0.0649	
PANCN0T01	pancreas, 29 M	3	0.0642	
PROSNOT14	prostate, 60 M, match to PROSTUT08	2	0.0512	
PANCN0T07	pancreas, fetal M	1	0.0287	
PROSNOT18	prostate, 58 M	1	0.0256	
ISLTN0T01	pancreas, islet cells, M/F	2	0.0251	
PROSNOT15	prostate, 66 M, match to PROSTUT10	1	0.0241	
BRSTN0T05	breast, 58 F, match to BRSTTUT03	1	0.0154	
PANCN0T05	pancreas, 2 M	1	0.0146	
PROSTUT04	prostate tumor, 57 M, match to PROSNOT06	1	0.0117	
LUNGAST01	lung, asthma, 17 M	1	0.0094	
PROSN0N01	prostate, 28 M, NORM	1	0.0094	
CARDFEM01	heart, fetal, NORM, WM	1	0.0083	

FIGURE 5